Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:02:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084342.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3084342 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084342.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:02:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084342.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,434,380
Mapped reads	2,256,071 / 92.68%
Unmapped reads	178,309 / 7.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,089 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	80,965 / 3.33%
Duplication rate	2.96%
Clipped reads	727,144 / 29.87%

2.2. ACGT Content

Number/percentage of A's	44,857,218 / 28.69%
Number/percentage of C's	28,811,820 / 18.43%
Number/percentage of T's	49,992,118 / 31.97%
Number/percentage of G's	32,478,291 / 20.77%
Number/percentage of N's	218,963 / 0.14%
GC Percentage	39.2%

2.3. Coverage

Mean	0.0505

Standard Deviation	0.3635

2.4. Mapping Quality

Mean Mapping Quality	47.43

2.5. Mismatches and indels

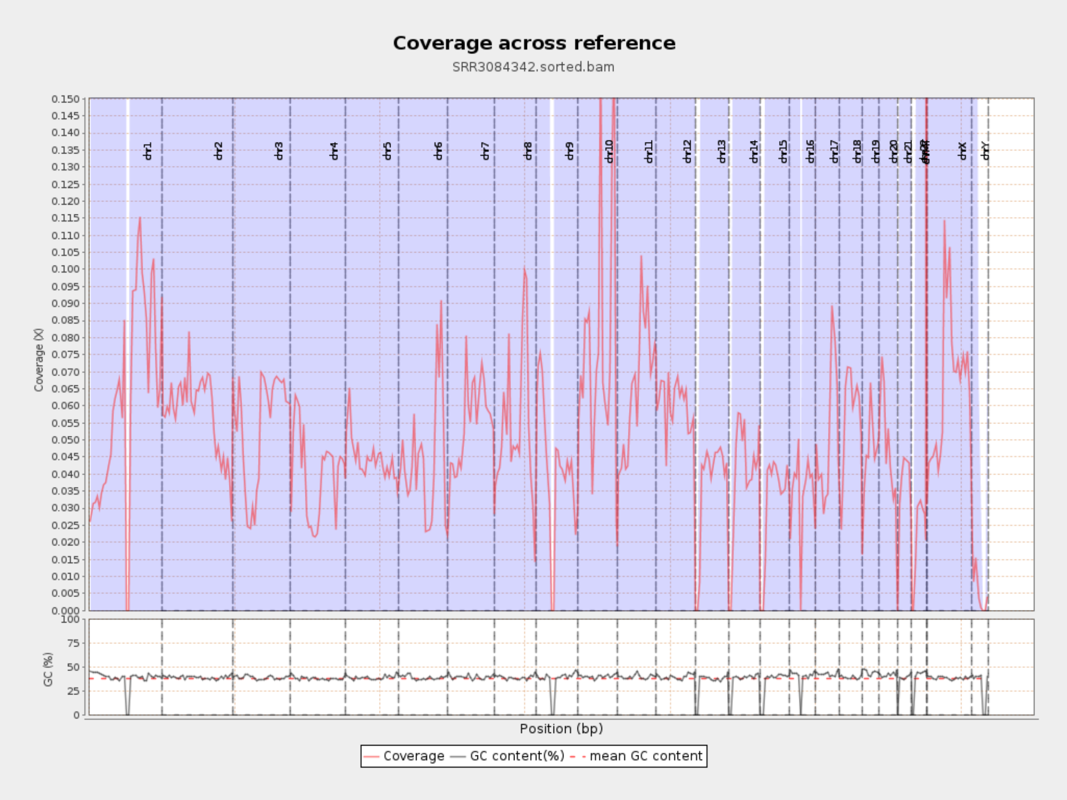
General error rate	0.95%
Mismatches	1,459,035
Insertions	11,241
Mapped reads with at least one insertion	0.49%
Deletions	32,315
Mapped reads with at least one deletion	1.42%
Homopolymer indels	48.48%

2.6. Chromosome stats

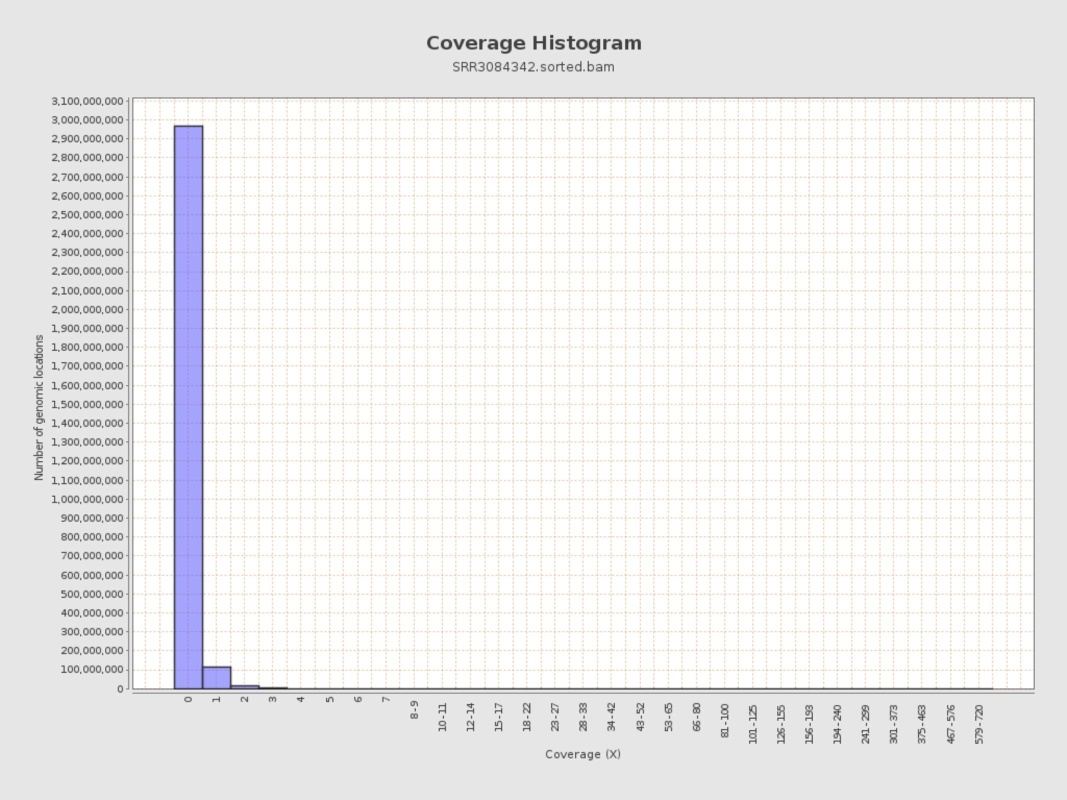
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15338237	0.0615	0.6448
chr2	243199373	14126452	0.0581	0.3786
chr3	198022430	10710038	0.0541	0.272
chr4	191154276	7701156	0.0403	0.2404
chr5	180915260	8090920	0.0447	0.2425
chr6	171115067	7536635	0.044	0.2645
chr7	159138663	8807335	0.0553	0.469

chr8	146364022	7871240	0.0538	0.4638
chr9	141213431	5911305	0.0419	0.3032
chr10	135534747	10919472	0.0806	0.4919
chr11	135006516	8808750	0.0652	0.3474
chr12	133851895	8026292	0.06	0.2835
chr13	115169878	4171361	0.0362	0.2181
chr14	107349540	4184691	0.039	0.2338
chr15	102531392	3273699	0.0319	0.2067
chr16	90354753	3128127	0.0346	0.2401
chr17	81195210	4164307	0.0513	0.2734
chr18	78077248	4449618	0.057	0.4999
chr19	59128983	2790642	0.0472	0.4167
chr20	63025520	3084810	0.0489	0.2598
chr21	48129895	1702931	0.0354	0.2301
chr22	51304566	1073710	0.0209	0.1629
chrMT	16571	14046	0.8476	1.2066
chrX	155270560	10190672	0.0656	0.3243
chrY	59373566	338224	0.0057	0.1259

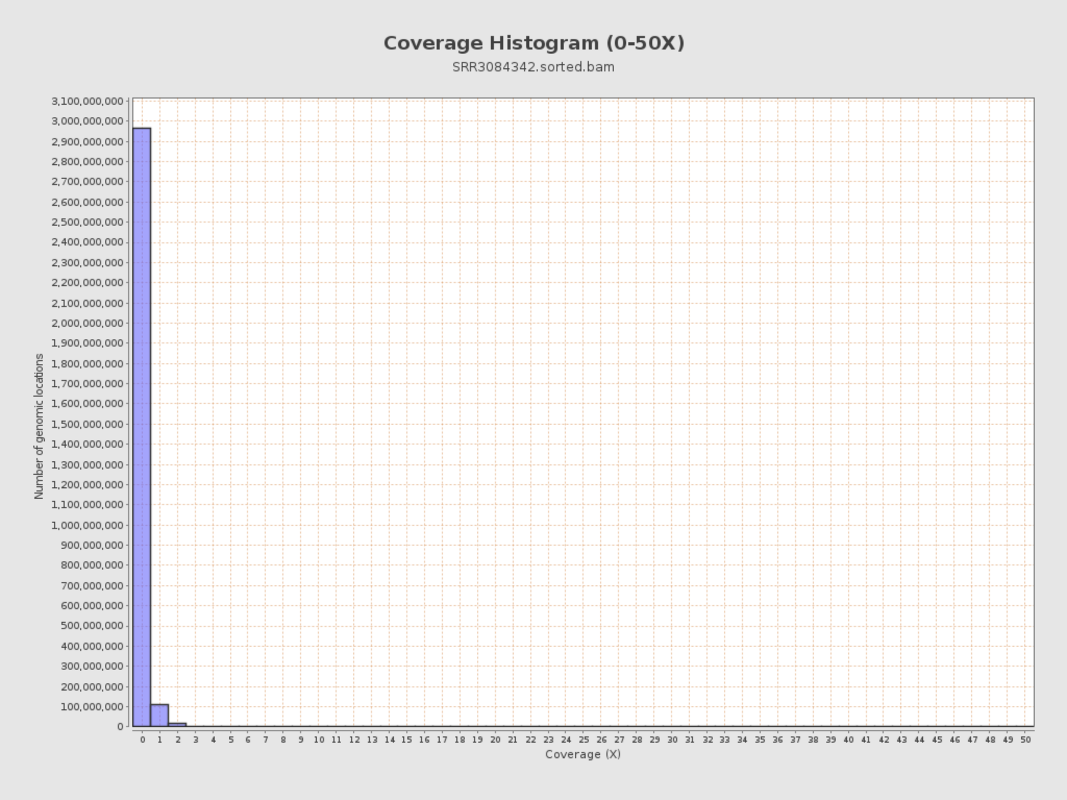
3. Results : Coverage across reference



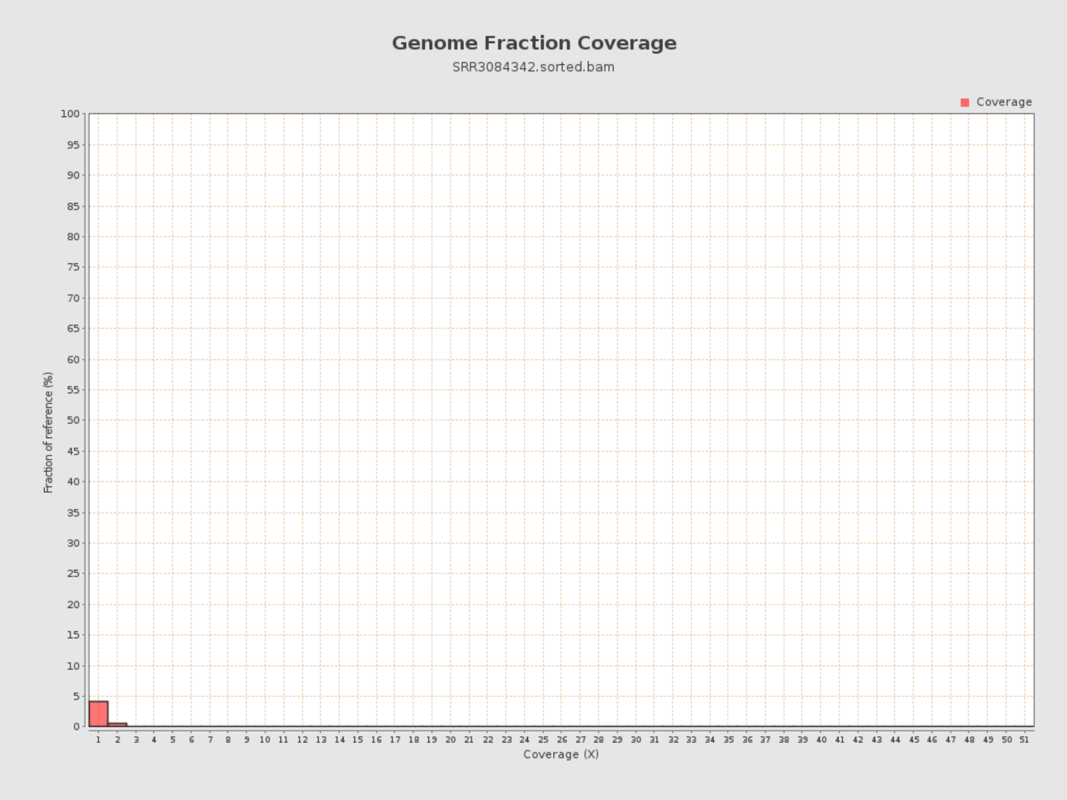
4. Results : Coverage Histogram



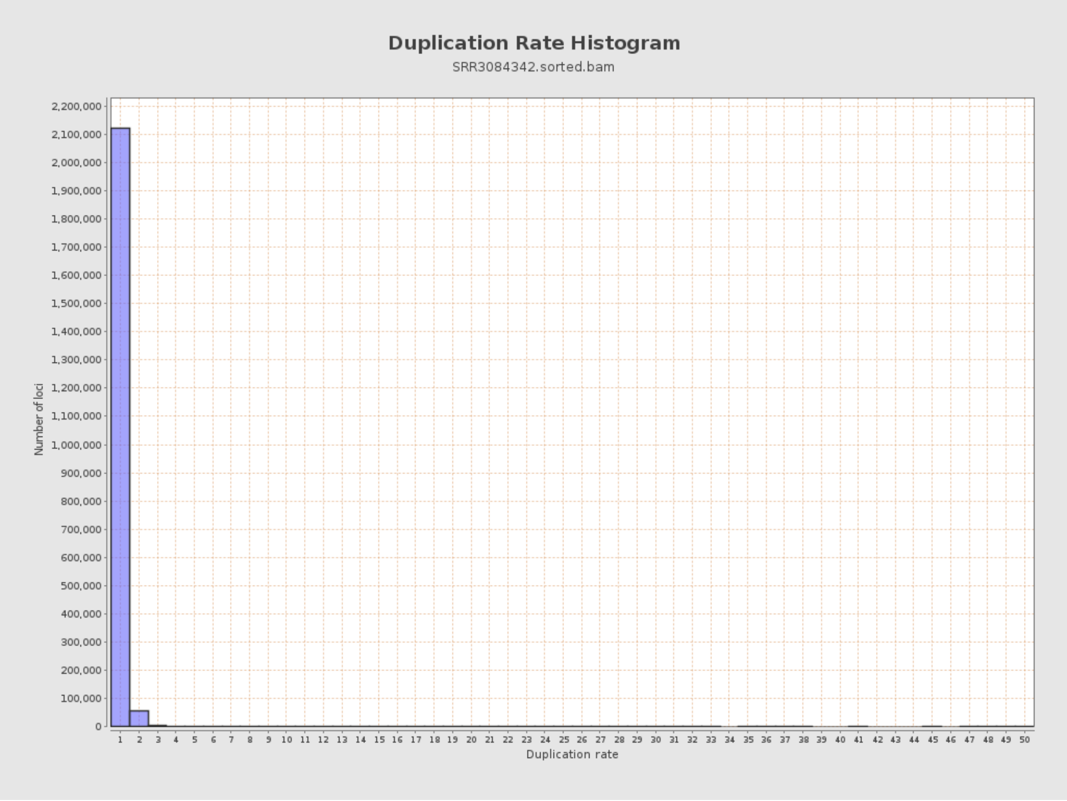
5. Results : Coverage Histogram (0-50X)



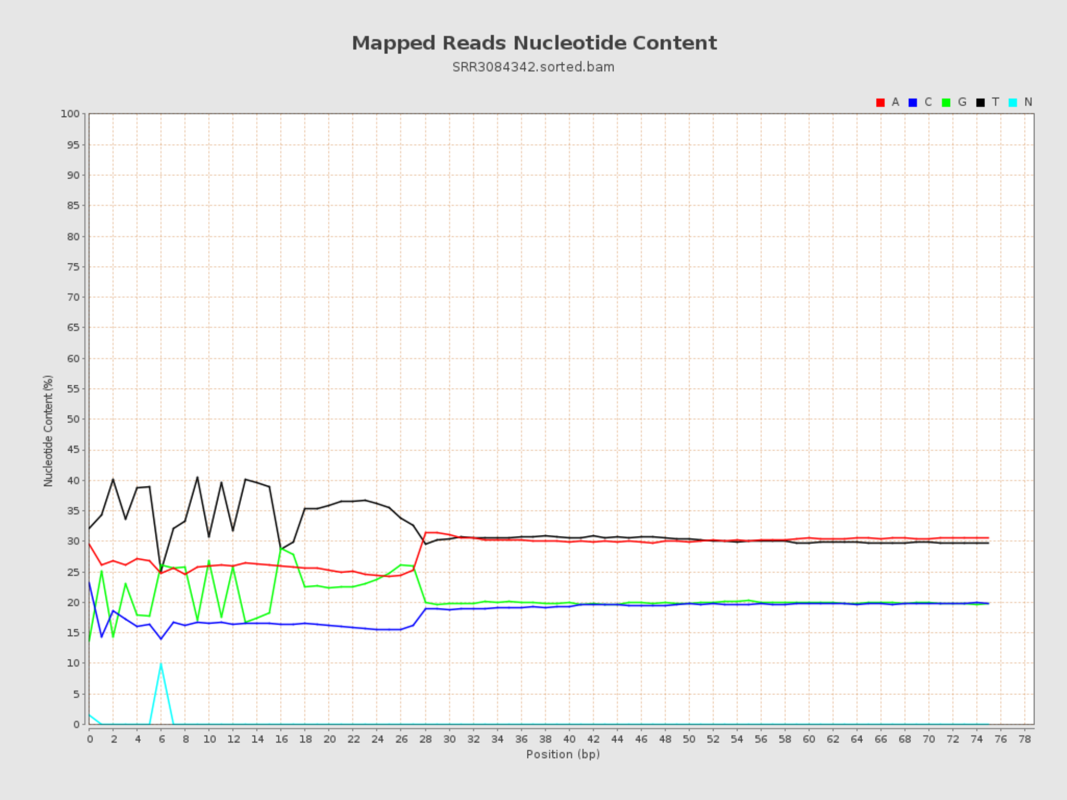
6. Results : Genome Fraction Coverage



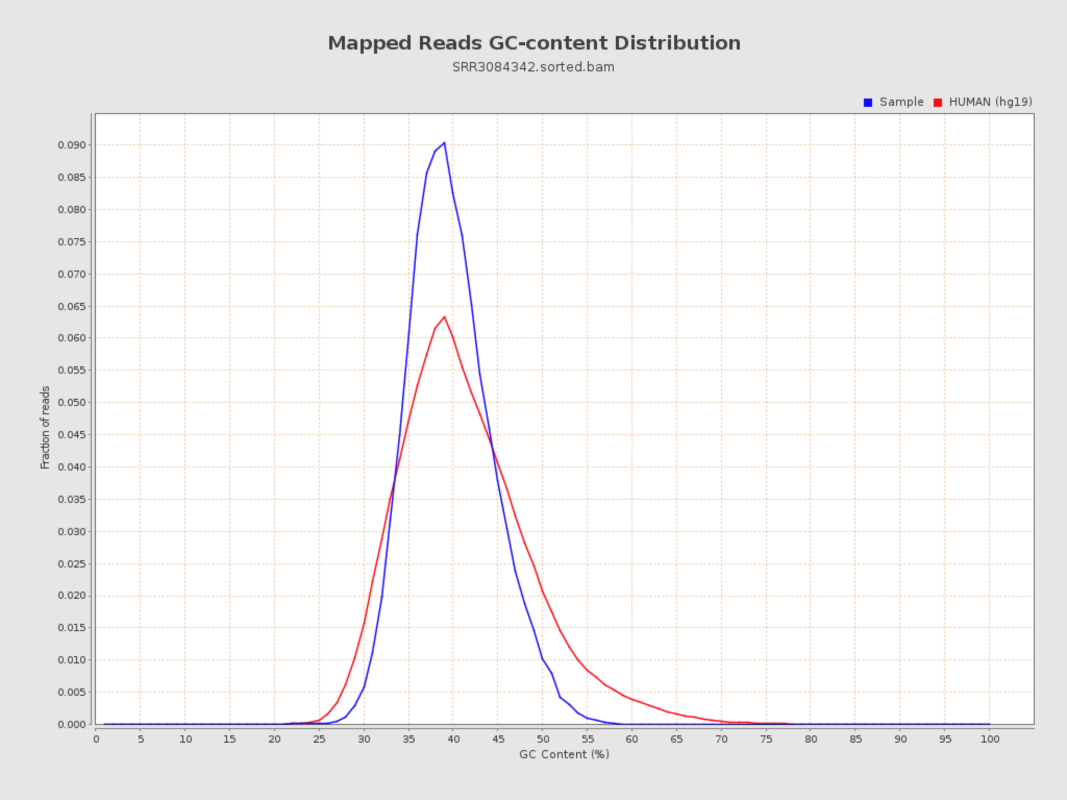
7. Results : Duplication Rate Histogram



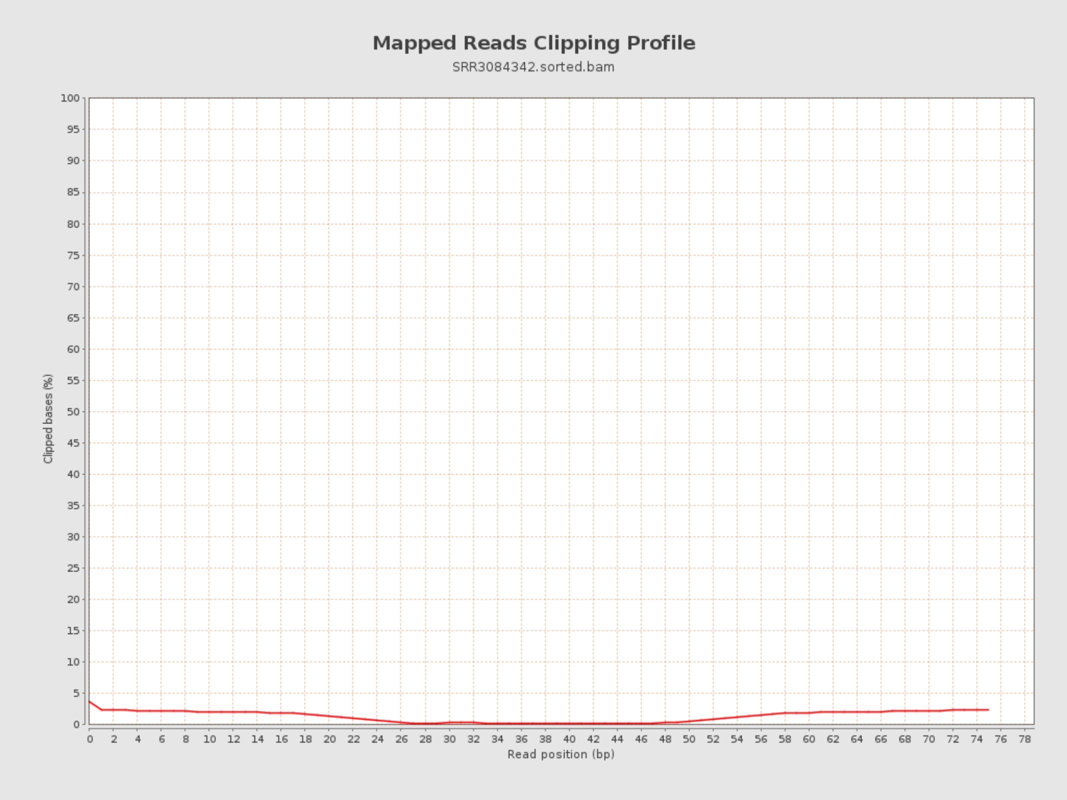
8. Results : Mapped Reads Nucleotide Content



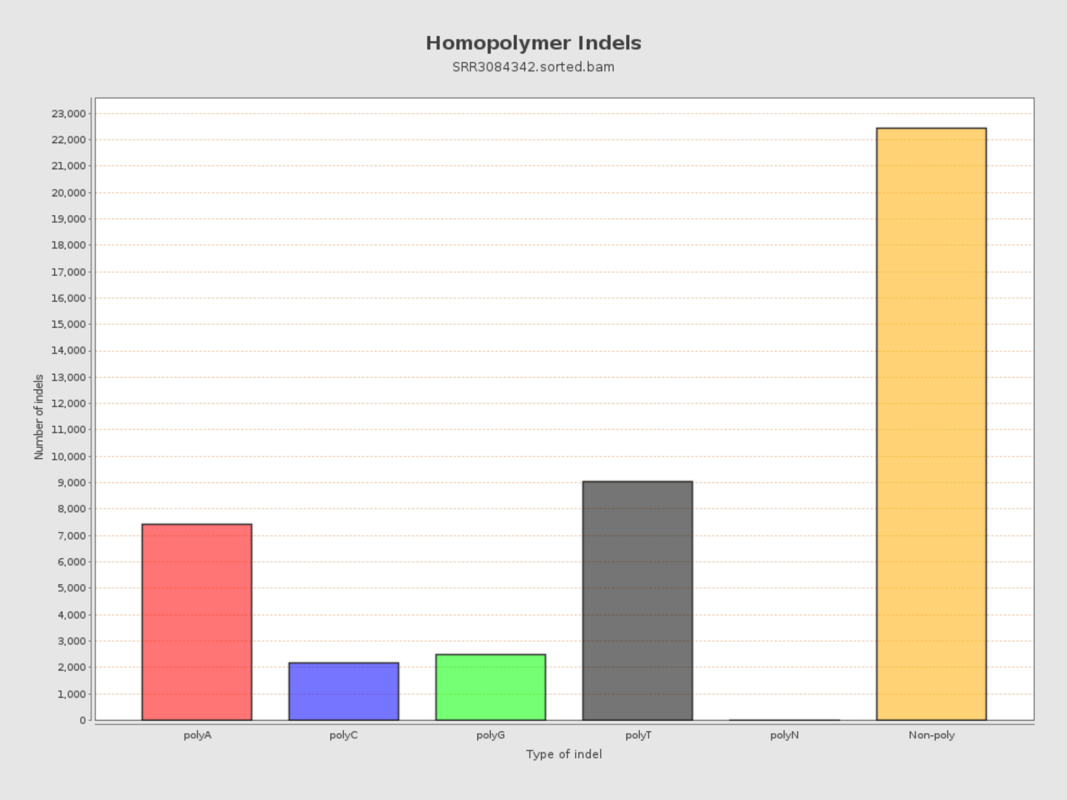
9. Results : Mapped Reads GC-content Distribution



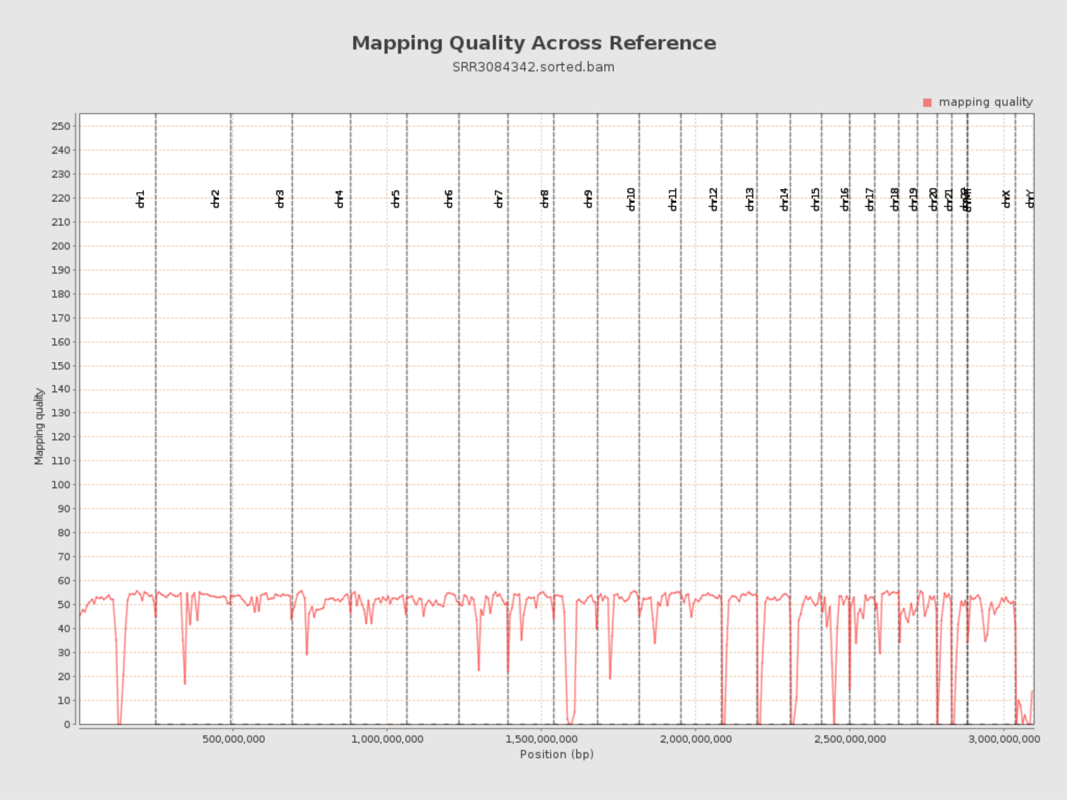
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram